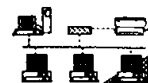


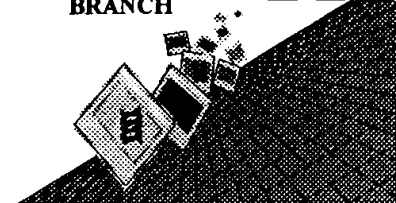
K. Schnizer

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING

ERROR REPORT



FILE COPY

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/247,874
Art Unit / Team No. : 1632
Date Processed by STIC: 6/15/89

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/247,874

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 ✓ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/247,874

DATE: 06/15/1999
TIME: 11:56:38

Input Set: I247874.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

*see
P. 5 and P. 4, to*

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2 di Giovine, Francesco Saverio
3 <120> TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC BASED ON A NOVEL IL-1B
4 MUTATION
5 <130> FILE REFERENCE: MSA-004.01
6 <140> CURRENT APPLICATION NUMBER: US/09/247,874
7 <141> CURRENT FILING DATE: 1999-02-10
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Does Not Comply
Corrected Diskette Needed

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RAW SEQUENCE LISTING
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176 gattgcttga gcccagaagt tcaagactgc agtgagctta tccgttgacc tgcaggtcga 9720
177 c 9721

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<210> SEQ ID NO 2

<211> LENGTH: 9721

<212> TYPE: DNA

<213> ORGANISM: IL-1Beta allele 2

<400> SEQUENCE: 2

W-->

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184 ggctctgagg aagggtggcag ttctacaac gggagaacca gtggttaatt tgcaagtg 120
185 new 10 atcctgtgga ggcanncaga ggagtcacct aggccacca gacagggtt ttagctatct 180
186 gcaggccaga caccaaattt caggagggtc cagtgttagg aatggattat ggcttatcaa 240
187 attcacagga aactaacatg ttgaacagct tttagatttc ctgtggaaaa tataacttac 300
188 taaagatgga gttcttgtga ctgactcctg atatcaagat actgggagcc aaattaaaaa 360
189 tcagaaggct gcttggagag caagtccatg aaatgctctt tttccacag tagaacctat 420
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192 agcagcaaac tctatctcac ctgaatgtac atgccaggca ctgtgctaga cttggctcaa 600
193 aaagatttca gtttctctga ggaaccagga gggcaagggt tcaactcagt gctataagaa 660
194 gtgttacagg ctggacacgg tggctcacgc ctgtaatccc aacatttggt aggccaggc 720

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PAGE: 5

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/247,874

DATE: 06/15/1999
TIME: 11:56:38

Input Set: I247874.RAW

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199      aaaagtgtta tgatgcagac ctgtcaaaga ggcaaaggag ggtgttccta cactccaggc 1020
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208      ccatttatcc atctgtaagt gggaagattc ctaaacttaa gtacaaagaa gtgaatgaag 1560
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION US/09/247,874

DATE: 06/15/1999

TIME: 11:56:38

Input Set: I247874.RAW

Line	? Error/Warning	Original Text
17	W "N" or "Xaa" used: Feature required	atcctgtgga ggcanncaga ggagtcccct aggccacc
185	W "N" or "Xaa" used: Feature required	atcctgtgga ggcanncaga ggagtcccct aggccacc
437	W "N" or "Xaa" used: Feature required	ccgactcgag nnnnnnatgt gg